WHAT IS CLAIMED IS:

1. A composition comprising:

(a) an isolated polypeptide comprising at least one LDL or VLDL nucleic acid binding domain; and

(b) a nucleic acid comprising an LDL or VLDL binding sequence,

wherein said nucleic acid is bound to said polypeptide.

2. The composition of claim 1, wherein said polypeptide comprises an LDL nucleic acid binding domain.

3. The composition of claim 1, wherein said polypeptide comprises a VLDL nucleic acid binding domain.

4. The composition of claim 1, wherein said nucleic acid comprises an expression region operably linked to a promoter active in eukaryotic cells.

5. The composition of claim 4, wherein said expression region encodes a polypeptide.

6. The composition of claim 4, wherein said expression region comprises an antisense construct.

7. The composition of claim 5, wherein said polypeptide is selected from the group consisting of α-globin, β-globin, γ-globin, granulocyte macrophage-colony stimulating factor (GM-CSF), tumor necrosis factor (TNF), IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, β-interferon, γ-interferon, cytosine deaminase, adenosine deaminase, β-glucuronidase, hypoxanthine guanine phosphoribosyl transferase, galactose-1-phosphate

uridyltransferase, glucocerbrosidase, glucose-6-phosphatase, thymidine kinase, lysosomal glucosidase, growth hormone, nerve growth factor, insulin, adrenocorticotropic hormone, parathormone, follicle-stimulating hormone, luteinizing hormone, epidermal growth factor, thyroid stimulating hormone of CFTR, EGFR, VEGFR, IL-2 receptor, estrogen receptor, Bax, Bak, Bcl-X_s, Bik, Bid, Bad, Harakiri, Ad E1B, an ICE-CED3 protease neomycin resistance, luciferase, adenine phosphoribosyl transferase (APRT), retinoblastoma, insulin, mast cell growth factor, p53, p16, p21, MMAC1, p73, zac1 and BRCAI.

8. The composition of claim 6, wherein said antisense construct is complementary to a segment of an oncogene.

9. The composition of claim 8, wherein said oncogene is selected from the group consisting of *ras, myc, neu, raf, erb, src, fms, jun, trk, ret, gsp, hst, bcl* and *abl.*

10. The composition of claim 4, wherein said promoter is selected from the group consisting of CMV IE, LTR, SV40 IE, HSV *tk*, β-actin, human globin α, human globin β and human globin γ promoter.

11. The composition of claim 1, wherein said nucleic acid binding domain is an apoB100 nucleic acid binding domain.

12. The composition of claim 1, wherein said composition further comprises one or more lipoproteins selected from the group consisting of apoA1, apoA-II, apoA-IV, acat, apoE, apoC-II, apoC-III and apo-D.

13. The composition of claim 11, wherein said apoB100 is selected from the group consisting of human, rat and baboon apoB100.

14. The composition of claim 1, wherein said polypeptide comprises at least two nucleic acid binding domains.

15. The composition of claim 14, wherein said nucleic acid binding domain contains a motif selected from the group consisting of a proline pipe helix DNA binding motif, a ISGF3γ-like DNA binding motif, a SREBP-like DNA binding motif, a coiled-coil motif and a nucleotide (ATP)-binding motif.

16. The composition of claim 14, wherein said binding domain is selected from the group consisting of SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, , SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166 and SEQ ID NO:175.

17. The composition of claim 1, wherein said polypeptide further comprises at least one nuclear localization sequence.

18. The composition of claim 17, wherein said nuclear localization sequence is from apoB100.

19. The composition of claim 17, wherein said nuclear localization sequence is selected from the group consisting of SEQ ID NO:178, SEQ ID NO: 179, SEQ ID

NO: 180, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210.

20. A method for expressing a polypeptide in a human cell comprising:

(a) providing a composition comprising (i) an isolated polypeptide comprising at least one LDL or VLDL nucleic acid binding domain and (ii) a nucleic acid comprising an expression cassette comprising a sequence encoding said polypeptide and a promoter active in eukaryotic cells, wherein said coding sequence is operably linked to said promoter, and wherein said nucleic acid sequence is bound to said LDL or VLDL;

b) contacting said composition with said cell under conditions permitting transfer of said composition into said cell; and

c) culturing said cell under conditions permitting the expression of said polypeptide.

21. The method of claim 20, wherein said polypeptide is a tumor suppressor.

22. The method of claim 20, wherein said polypeptide is a cytokine.

23. The method of claim 20, wherein said polypeptide is an enzyme.

24. The method of claim 20, wherein said polypeptide is a hormone.

25. The method of claim 20, wherein said polypeptide is a receptor.

26. The method of claim 20, wherein said polypeptide is an inducer of apoptosis.

27. The method of claim 21, wherein said tumor suppressor is selected from the group consisting of p53, p16, p21, MMAC1, p73, zac1, BRCAI and Rb.

28. The method of claim 22, wherein said cytokine is selected from the group consisting of IL-2, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, TNF, GMCSF, β-interferon and γ-interferon.

29. The method of claim 23, wherein said enzyme is selected from the group consisting of cytosine deaminase, adenosine deaminase, β-glucuronidase, hypoxanthine guanine phosphoribosyl transferase, galactose-1-phosphate uridyltransferase, glucocerbrosidase, glucose-6-phosphatase, thymidine kinase and lysosomal glucosidase.

30. The method of claim 24, wherein said hormone is selected from the group consisting of growth hormone, nerve growth factor, insulin, adrenocorticotropic hormone, parathormone, follicle-stimulating hormone, luteinizing hormone, epidermal growth factor and thyroid stimulating hormone.

31. The method of claim 25, wherein said receptor is selected from the group consisting of CFTR, EGFR, VEGFR, IL-2 receptor and the estrogen receptor.

32. The method of claim 26, wherein said inducer of apoptosis is selected from the group consisting of Bax, Bak, Bcl-X_s, Bik, Bid, Bad, Harakiri, Ad E1B and an ICE-CED3 protease.

33. The method of claim 20, wherein said promoter is selected from the group consisting of CMV IE, LTR, SV40 IE, HSV *tk*, β-actin, human globin α, human globin β and human globin γ promoter.

34. The method of claim 20, wherein said nucleic acid binding domain is an apoB100 nucleic acid binding domain.

35. The method of claim 20, wherein said apoB100 is selected from the group consisting of human, rat and baboon low density apoB100.

36. The method of claim 27, wherein said binding region is selected from the group consisting of a proline pipe helix DNA binding motif, a ISGF3γ-like DNA binding motif, a SREBP-like DNA binding motif, a coiled-coil motifs, and a nucleotide (ATP)-binding motif.

37. The method of claim 20, wherein said polypeptide further comprises at least one nuclear localization sequence.

38. The method of claim 37, wherein said nuclear localization sequence is an apoB100 nuclear localization sequence.

39. The method of claim 20, wherein said polypeptide is selected from the group consisting of α-globin, β-globin, γ-globin, neomycin resistance, luciferase, adenine phosphoribosyl transferase (APRT), mast cell growth factor.

40. A method for providing an expression construct to a human cell comprising:

(a) providing a composition comprising (i) an isolated polypeptide comprising at least one LDL or VLDL nucleic acid binding domain and (ii) an

expression cassette comprising a nucleic acid sequence encoding an expression region and a promoter active in eukaryotic cells, wherein said expression region is operably linked to said promoter, and wherein said nucleic acid sequence is bound to said LDL or VLDL;

b) contacting said composition with said cell under conditions permitting transfer of said composition into said cell; and

c) culturing said cell under conditions permitting the expression of said expression region.

41. The method of claim 40, wherein said expression construct comprises an antisense construct.

42. The method of claim 40, wherein said antisense construct is derived from an oncogene.

43. The method of claim 42, wherein said oncogene is selected from the group consisting *ras, myc, neu, raf, erb, src, fms, jun, trk, ret, gsp, hst, bcl* and *abl*.

44. The method of claim 40, wherein said expression construct comprises a nucleic acid coding for a gene.

45. The method of claim 44, wherein said gene encodes a polypeptide.

46. The method of claim 40, wherein said promoter is selected from the group consisting of CMV IE, LTR, SV40 IE, HSV *tk*, β-actin, human globin α, human globin β and human globin γ promoter.

47. The method of claim 40, wherein said nucleic acid binding domain is an apoB100 nucleic acid binding domain.

48. The method of claim 47, wherein said apoB100 is selected from the group consisting of human, rat and baboon low density apoB100.

49. The method of claim 48, wherein said DNA binding region is selected from the group consisting of a proline pipe helix DNA binding motif, a ISGF3γ-like DNA binding motif, a SREBP-like DNA binding motif, a coiled-coil motifs, and a nucleotide (ATP)-binding motif.

50. The method of claim 40, wherein said polypeptide further comprises at least one nuclear localization sequence.

51. The method of claim 50, wherein said nuclear localization sequence is an apoB100 nuclear localization sequence.

52. The method of claim 40, wherein said gene encodes a polypeptide selected from the group consisting of α-globin, β-globin, γ-globin, green fluorescent protein, neomycin resistance, luciferase, adenine phosphoribosyl transferase (APRT), mast cell growth factor.

53. A method for treating a human disease comprising:

a) providing a composition comprising (i) an isolated polypeptide comprising at least one LDL or VLDL nucleic acid binding domain and (ii) an expression cassette comprising a nucleic acid sequence encoding an expression region and a promoter active in eukaryotic cells, wherein said expression region is operably linked to said promoter, and wherein said nucleic acid sequence is bound to said LDL or VLDL; and

b) administering said composition to a human subject having said disease under conditions permitting transfer of said composition into cells of said human subject.

54. The method of claim 53, wherein said disease is selected from the group consisting of cancer, diabetes, cystic fibrosis and arteriosclerosis.

55. The method of claim 53, wherein said promoter is selected from the group consisting of CMV IE, LTR, SV40 IE, HSV *tk*, β-actin, human globin α, human globin β and human globin γ promoter.

56. The method of claim 53, wherein said nucleic acid binding domain is an apoB100 binding domain.

57. The method of claim 56, wherein said apoB100 is selected from the group consisting of human, rat and baboon low density lipoprotein apoB100.

58. The method of claim 53, wherein said polypeptide comprises at least two nucleic acid binding regions.

59. The method of claim 58, wherein said binding region is selected from the group consisting of a proline pipe helix DNA binding motif, a ISGF3γ-like DNA binding motif, a SREBP-like DNA binding motif, a coiled-coil motifs, and a nucleotide (ATP)-binding motif.

60. The method of claim 53, wherein said polypeptide comprises at least one nuclear localization sequence.

61. The method of claims 60, wherein said nuclear localization sequence is an apoB100 nuclear localization sequence.

62. The method of claim 53, wherein said nucleic acid encodes a gene.

63. The method of claim 53, wherein said expression construct comprises an antisense construct.

64. A pharmaceutical composition comprising:

(a) an isolated polypeptide comprising at least one LDL or VLDL nucleic acid binding domain; and

(b) a nucleic acid comprising an LDL or VLDL binding sequence, wherein said nucleic acid is bound to said polypeptide;

said pharmaceutical composition being dispersed in a suitable diluent.

65. A method of transforming a cell comprising:

a) providing a cell;

b) contacting said cell with a composition comprising (i) an isolated polypeptide comprising at least one LDL or VLDL nucleic acid binding domain and (ii) an expression cassette comprising a nucleic acid sequence encoding an expression region and a promoter active in eukaryotic cells, wherein said expression region is operably linked to said promoter, and wherein said nucleic acid sequence is bound to said LDL or VLDL;

wherein expression of said expression region is indicative of said transformation.

66. A method of transfecting a cell comprising the steps of:

a) providing a cell;

b) contacting said cell with a composition comprising (i) an isolated polypeptide comprising at least one LDL or VLDL nucleic acid binding domain and (ii) an expression cassette comprising a nucleic acid sequence encoding an

expression region and a promoter active in eukaryotic cells, wherein said expression region is operably linked to said promoter, and wherein said nucleic acid sequence is bound to said LDL or VLDL; and

wherein expression of said expression region is indicative of said transfection.

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